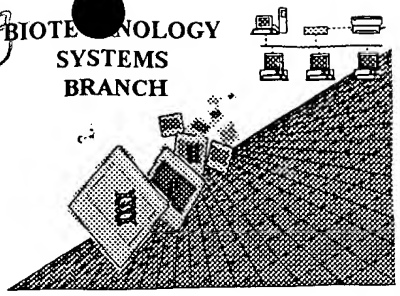
Fran, Young

BIOTECHNOLOGY SYSTEMS BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/744,910A

Source: PCT/09

Date Processed by STIC: 6/12/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED **SUGGESTED CORRECTION** **SERIAL NUMBER:** 09/944,910A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____	Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2__J__	Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3__J__	Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4____	Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5____	Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6____	PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7____	Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8____	Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9____	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10____	Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11____	Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12____	PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

PCT

RAW SEQUENCE LISTING DATE: 06/12/2001
PATENT APPLICATION: US/09/744,910A TIME: 11:30:52

Does Not Comply
Corrected Diskette Needed

Input Set : A:\PTO.txt
Output Set: N:\CRF3\06112001\I744910A.raw

```
      3 <110> APPLICANT: ASAHIKASEI KOGYO KABUSIKI KAISHA
      5 <120> TITLE OF INVENTION: Antibodies for Detecting Microorganisms
      7 <130> FILE REFERENCE: ASAHI-2
C-->  9 <140> CURRENT APPLICATION NUMBER: US/09/744,910A
C-->  9 <141> CURRENT FILING DATE: 2001-05-17
      9 <150> PRIOR APPLICATION NUMBER: JP 10/230204
W--> 10 <151> PRIOR FILING DATE: 1998-7-31
     12 <160> NUMBER OF SEQ ID NOS: 22
```

1998-07-31 use this date format

ERRORED SEQUENCES

```
     52 <210> SEQ ID NO: 2
     53 <211> LENGTH: 123
     54 <212> TYPE: PRT
     55 <213> ORGANISM: Haemophilus influenzae
     57 <400> SEQUENCE: 2
     58 Met Ser Leu Thr Asn Glu Gln Ile Ile Glu Ala Ile Ala Ser Lys Thr
E--> 59  1               5                  10                  15
     60 Val Thr Glu Ile Val Glu Leu Ile Ala Ala Met Glu Glu Lys Phe Gly
E--> 61          20                  25                  30
     62 Val Ser Ala Ala Ala Ala Val Ala Ala Ala Pro Ala Ala Gly Gly Ala
E--> 63      35                  40                  45
     64 Ala Ala Ala Glu Glu Lys Thr Glu Phe Asp Val Val Leu Lys Ser Ala
E--> 65  50                  55                  60
     66 Gly Ala Asn Lys Val Ala Val Ile Lys Ala Val Arg Gly Ala Thr Gly
E--> 67 65                  70                  75                  80
     68 Leu Gly Leu Lys Glu Ala Lys Asp Leu Val Glu Ser Ala Pro Ala Asn
E--> 69              85                  90                  95
     70 Leu Lys Glu Gly Val Ser Lys Glu Glu Ala Glu Ala Leu Lys Lys Glu
E--> 71          100                 105                 110
     72 Leu Glu Glu Ala Gly Ala Glu Val Glu Val Lys
E--> 73      115                 120
```

misaligned amino acid nos. (see item 3 on Error Summary Sheet)

```
    113 <210> SEQ ID NO: 4
    114 <211> LENGTH: 125
    115 <212> TYPE: PRT
    116 <213> ORGANISM: Helicobacter pylori
    118 <400> SEQUENCE: 4
    119 Met Ala Ile Ser Lys Glu Glu Val Leu Glu Tyr Ile Gly Ser Leu Ser
E--> 120  1               5                  10                  15
    121 Val Leu Glu Leu Ser Glu Leu Val Lys Met Phe Glu Glu Lys Phe Gly
E--> 122          20                  25                  30
    123 Val Ser Ala Thr Pro Thr Val Val Ala Gly Ala Ala Val Ala Gly Gly
E--> 124      35                  40                  45
    125 Ala Ala Ala Glu Ser Glu Glu Lys Thr Glu Phe Asn Val Ile Leu Ala
E--> 126  50                  55                  60
    127 Asp Ser Gly Ala Glu Lys Ile Lys Val Ile Lys Val Val Arg Glu Ile
```

same error

RAW SEQUENCE LISTING DATE: 06/12/2001
PATENT APPLICATION: US/09/744,910A TIME: 11:30:52

Input Set : A:\PTO.txt
Output Set: N:\CRF3\06112001\I744910A.raw

```
E--> 128 65                  70                  75                  80
     129 Thr Gly Leu Gly Leu Lys Glu Ala Lys Asp Ala Thr Glu Lys Thr Pro
E--> 130               85                  90                  95
     131 His Val Leu Lys Glu Gly Val Asn Lys Glu Glu Ala Glu Thr Ile Lys
E--> 132            100                 105                 110
     133 Lys Lys Leu Glu Glu Val Gly Ala Lys Val Glu Val Lys
E--> 134        115                 120                 125
     174 <210> SEQ ID NO: 6
     175 <211> LENGTH: 122
     176 <212> TYPE: PRT
     177 <213> ORGANISM: Streptococcus pneumoniae
     179 <400> SEQUENCE: 6
     180 Met Ala Leu Asn Ile Glu Asn Ile Ile Ala Glu Ile Lys Glu Ala Ser
E--> 181  1               5                  10                  15
     182 Ile Leu Glu Leu Asn Asp Leu Val Lys Ala Ile Glu Glu Glu Phe Gly
E--> 183            20                  25                  30
     184 Val Thr Ala Ala Ala Pro Val Ala Val Ala Ala Ala Asp Ala Ala Asp
E--> 185        35                  40                  45
     186 Ala Gly Ala Ala Lys Asp Ser Phe Asp Val Glu Leu Thr Ser Ala Gly
E--> 187     50                  55                  60
     188 Asp Lys Lys Val Gly Val Ile Lys Val Val Arg Glu Ile Thr Gly Leu
E--> 189 65                  70                  75                  80
     190 Gly Leu Lys Glu Ala Lys Glu Leu Val Asp Gly Ala Pro Ala Leu Val
E--> 191               85                  90                  95
     192 Lys Glu Gly Val Ala Thr Ala Glu Ala Glu Glu Ile Lys Ala Lys Leu
E--> 193            100                 105                 110
     194 Glu Glu Ala Gly Ala Ser Val Thr Leu Lys
E--> 195        115                 120
     235 <210> SEQ ID NO: 8
     236 <211> LENGTH: 123
     237 <212> TYPE: PRT
     238 <213> ORGANISM: Neisseria gonorrhoeae
     240 <400> SEQUENCE: 8
     241 Met Ala Ile Thr Lys Glu Asp Ile Leu Glu Ala Val Gly Ser Leu Thr
E--> 242  1               5                  10                  15
     243 Val Met Glu Leu Asn Asp Leu Val Lys Ala Phe Glu Glu Lys Phe Gly
E--> 244            20                  25                  30
     245 Val Ser Ala Ala Ala Val Ala Val Ala Gly Pro Ala Gly Ala Gly Ala
E--> 246        35                  40                  45
     247 Ala Asp Ala Glu Glu Lys Thr Glu Phe Asp Val Val Leu Ala Ser Ala
E--> 248     50                  55                  60
     249 Gly Asp Gln Lys Val Gly Val Ile Lys Val Val Arg Ala Ile Thr Gly
E--> 250 65                  70                  75                  80
     251 Leu Gly Leu Lys Glu Ala Lys Asp Ile Val Asp Gly Ala Pro Lys Thr
E--> 252               85                  90                  95
     253 Ile Lys Glu Gly Val Ser Lys Ala Glu Ala Glu Asp Ile Gln Lys Gln
E--> 254            100                 105                 110
     255 Leu Glu Ala Ala Gly Ala Lys Val Glu Ile Lys
E--> 256        115                 120
```

same

same

same

RAW SEQUENCE LISTING DATE: 06/12/2001
PATENT APPLICATION: US/09/744,910A TIME: 11:30:52

Input Set : A:\PTO.txt
Output Set: N:\CRF3\06112001\I744910A.raw

296 <210> SEQ ID NO: 10
297 <211> LENGTH: 123
298 <212> TYPE: PRT
299 <213> ORGANISM: Neisseria menigitidis
301 <400> SEQUENCE: 10
302 Met Ala Ile Thr Lys Glu Asp Ile Leu Glu Ala Val Gly Ser Leu Thr
E--> 303 1 5 10 15
304 Val Met Glu Leu Asn Asp Leu Val Lys Ala Phe Glu Glu Lys Phe Gly
E--> 305 20 25 30
306 Val Ser Ala Ala Ala Val Ala Val Ala Gly Pro Ala Gly Ala Gly Ala
E--> 307 35 40 45
308 Ala Asp Ala Glu Glu Lys Thr Glu Phe Asp Val Val Leu Ala Ser Ala
E--> 309 50 55 60
310 Gly Asp Gln Lys Val Gly Val Ile Lys Val Val Arg Ala Ile Thr Gly
E--> 311 65 70 75 80
312 Leu Gly Leu Lys Glu Ala Lys Asp Ile Val Asp Gly Ala Pro Lys Thr
E--> 313 85 90 95
314 Ile Lys Glu Gly Val Ser Lys Ala Glu Ala Glu Asp Ile Gln Lys Gln
E--> 315 100 105 110
316 Leu Glu Glu Ala Gly Ala Lys Val Glu Ile Lys
E--> 317 115 120
319 <210> SEQ ID NO: 11
320 <211> LENGTH: (31) 30 shows
321 <212> TYPE: DNA
322 <213> ORGANISM: artificial sequence
324 <220> FEATURE:
325 <223> OTHER INFORMATION: The primers DNA for PCR used to acquire the ribosomal protein L7/L12
326 gene from H. influenzae.
328 <400> SEQUENCE: 11
E--> 329 gtaaggatcc atgtcattaa ctaacgaaca (31) 30
367 <210> SEQ ID NO: 15
368 <211> LENGTH: (31) 30
369 <212> TYPE: DNA
370 <213> ORGANISM: artificial sequence
372 <220> FEATURE:
373 <223> OTHER INFORMATION: The primers DNA for PCR used to acquire the ribosomal protein L7/L12
374 gene from N. gonorrhoeae.
376 <400> SEQUENCE: 15
E--> 377 gtaaggatccatggctattactaaagaaga (31) 30
429 <210> SEQ ID NO: 18
430 <211> LENGTH: 123
431 <212> TYPE: PRT
432 <213> ORGANISM: Haemophilus influenzae
434 <400> SEQUENCE: 18
435 Met Ser Leu Thr Asn Glu Gln Ile Ile Glu Ala Ile Ala Ser Lys Thr
E--> 436 1 5 10 15
437 Val Thr Glu Ile Val Glu Leu Ile Ala Ala Met Glu Glu Lys Phe Gly
E--> 438 20 25 30
439 Val Ser Ala Ala Ala Ala Val Ala Ala Ala Pro Ala Ala Gly Gly Ala

same

Per 1.822 of Sequence Rules, group non-coding bases into 10's, with a space between each group

misaligned amino acid nos.

RAW SEQUENCE LISTING DATE: 06/12/2001
PATENT APPLICATION: US/09/744,910A TIME: 11:30:52

Input Set : A:\PTO.txt
Output Set: N:\CRF3\06112001\I744910A.raw

```
E--> 440        35                  40                  45
     441 Ala Ala Ala Glu Glu Lys Thr Glu Phe Asp Val Val Leu Lys Ser Ala
E--> 442     50                  55                  60
     443 Gly Ala Asn Lys Val Ala Val Ile Lys Ala Val Arg Gly Ala Thr Gly
E--> 444 65                  70                  75                  80
     445 Leu Gly Leu Lys Glu Ala Lys Asp Leu Val Glu Ser Ala Pro Ala Asn
E--> 446                 85                  90                  95
     447 Leu Lys Glu Gly Val Ser Lys Glu Glu Ala Glu Ala Leu Lys Lys Glu
E--> 448             100                 105                 110
     449 Leu Glu Glu Ala Gly Ala Glu Val Glu Val Lys
E--> 450         115                 120
     490 <210> SEQ ID NO: 20
     491 <211> LENGTH: 122
     492 <212> TYPE: PRT
     493 <213> ORGANISM: Streptococcus pneumoniae
     495 <400> SEQUENCE: 20
     496 Met Ala Leu Asn Ile Glu Asn Ile Ile Ala Glu Ile Lys Glu Ala Ser
E--> 497  1               5                  10                  15
     498 Ile Leu Glu Leu Asn Asp Leu Val Lys Ala Ile Glu Glu Glu Phe Gly
E--> 499             20                  25                  30
     500 Val Thr Ala Ala Ala Pro Val Ala Val Ala Ala Ala Asp Ala Ala Asp
E--> 501         35                  40                  45
     502 Ala Gly Ala Ala Lys Asp Ser Phe Asp Val Glu Leu Thr Ser Ala Gly
E--> 503     50                  55                  60
     504 Asp Lys Lys Val Gly Val Ile Lys Val Val Arg Glu Ile Thr Gly Leu
E--> 505 65                  70                  75                  80
     506 Gly Leu Lys Glu Ala Lys Glu Leu Val Asp Gly Ala Pro Ala Leu Val
E--> 507                 85                  90                  95
     508 Lys Glu Gly Val Ala Thr Ala Glu Ala Glu Glu Ile Lys Ala Lys Leu
E--> 509             100                 105                 110
     510 Glu Glu Ala Gly Ala Ser Val Thr Leu Lys
E--> 511         115                 120
     551 <210> SEQ ID NO: 22
     552 <211> LENGTH: 123
     553 <212> TYPE: PRT
     554 <213> ORGANISM: Neisseria gonorrhoeae
     556 <400> SEQUENCE: 22
     557 Met Ala Ile Thr Lys Glu Asp Ile Leu Glu Ala Val Gly Ser Leu Thr
E--> 558  1               5                  10                  15
     559 Val Met Glu Leu Asn Asp Leu Val Lys Ala Phe Glu Glu Lys Phe Gly
E--> 560             20                  25                  30
     561 Val Ser Ala Ala Ala Val Ala Val Ala Gly Pro Ala Gly Ala Gly Ala
E--> 562         35                  40                  45
     563 Ala Asp Ala Glu Glu Lys Thr Glu Phe Asp Val Val Leu Ala Ser Ala
E--> 564     50                  55                  60
     565 Gly Asp Gln Lys Val Gly Val Ile Lys Val Val Arg Ala Ile Thr Gly
E--> 566 65                  70                  75                  80
     567 Leu Gly Leu Lys Glu Ala Lys Asp Ile Val Asp Gly Ala Pro Lys Thr
E--> 568                 85                  90                  95
```

same

same
error

same

(see next page)

RAW SEQUENCE LISTING DATE: 06/12/2001
PATENT APPLICATION: **US/09/744,910A** TIME: 11:30:52

Input Set : **A:\PTO.txt**
Output Set: **N:\CRF3\06112001\I744910A.raw**

569 Ile Lys Glu Gly Val Ser Lys Ala Glu Ala Glu Asp Ile Gln Lys Gln
E--> 570 100 105 110
571 Leu Glu Ala Ala Gly Ala Lys Val Glu Ile Lys
E--> 572 115 120

same
error

VERIFICATION SUMMARY DATE: 06/12/2001
PATENT APPLICATION: **US/09/744,910A** TIME: 11:30:53

Input Set : **A:\PTO.txt**
Output Set: **N:\CRF3\06112001\I744910A.raw**

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:10 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:22 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:26 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:30 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:34 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:38 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:42 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:46 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:50 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:59 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
M:332 Repeated in SeqNo=2
L:83 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:87 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:91 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:95 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:99 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:103 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:107 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:120 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
M:332 Repeated in SeqNo=4
L:144 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:148 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:152 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:156 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:160 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:164 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:168 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:172 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:181 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6
M:332 Repeated in SeqNo=6
L:205 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:209 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:213 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:217 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:221 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:225 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:229 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:233 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:242 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
M:332 Repeated in SeqNo=8
L:266 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:270 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:274 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:278 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:282 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9

VERIFICATION SUMMARY DATE: 06/12/2001
PATENT APPLICATION: **US/09/744,910A** TIME: 11:30:53

Input Set : **A:\PTO.txt**
Output Set: **N:\CRF3\06112001\I744910A.raw**

L:286 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:290 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:294 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:303 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
M:332 Repeated in SeqNo=10
L:329 M:254 E: No. of Bases conflict, LENGTH:Input:31 Counted:30 SEQ:11
L:329 M:252 E: No. of Seq. differs, <211>LENGTH:Input:31 Found:30 SEQ:11
L:377 M:254 E: No. of Bases conflict, LENGTH:Input:31 Counted:30 SEQ:15
L:377 M:252 E: No. of Seq. differs, <211>LENGTH:Input:31 Found:30 SEQ:15
L:399 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:403 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:407 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:411 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:415 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:419 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:423 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:427 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:436 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:18
M:332 Repeated in SeqNo=18
L:460 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:464 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:497 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:20
M:332 Repeated in SeqNo=20
L:558 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
M:332 Repeated in SeqNo=22